TEAM 3

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/804,166*

DATE: 04/10/97
TIME: 08:46:56

INPUT SET: S16859.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                                SEQUENCE LISTING
 2
 3    (1)      General Information:
 4
 5         (i) APPLICANT: Campbell, Robert K.
 6                        Jameson, Bradford A.
 7                        Chappel, Scott C.
 8
 9        (ii) TITLE OF INVENTION: HYBRID PROTEINS
10
11       (iii) NUMBER OF SEQUENCES: 22
12
13        (iv) CORRESPONDENCE ADDRESS:
14             (A) ADDRESSEE: BROWDY AND NEIMARK
15             (B) STREET: 419 Seventh Street N.W., Ste. 300
16             (C) CITY: Washington
17             (D) STATE: D.C.
18             (E) COUNTRY: USA
19             (F) ZIP: 22207
20
21         (v) COMPUTER READABLE FORM:
22             (A) MEDIUM TYPE: Floppy disk
23             (B) COMPUTER: IBM PC compatible
24             (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25             (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26             _____
27    (vii) (vi) PRIOR APPLICATION DATA:
28             (A) APPLICATION NUMBER:  60/011,936
29             (B) FILING DATE:   20 February 1996
30             (C) CLASSIFICATION:
31
32      (viii) ATTORNEY/AGENT INFORMATION:
33             (A) NAME: Browdy, Roger L.
34             (B) REGISTRATION NUMBER: 25,618
35             (C) REFERENCE/DOCKET NUMBER: CAMPBELL=2A
36
37        (ix) TELECOMMUNICATION INFORMATION:
38             (A) TELEPHONE: (202) 628-5197
39             (B) TELEFAX: (202) 737-3528
40
41    (2) INFORMATION FOR SEQ ID NO:1:
42
43         (i) SEQUENCE CHARACTERISTICS:
44             (A) LENGTH: 1049 base pairs
45             (B) TYPE: nucleic acid
46             (C) STRANDEDNESS: single
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Does Not Comply Corrected Diskette Needed

insert
(vi) CURR. APP. DATA:
heading and
subheadings

INPUT SET: S16859.raw

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47                  (D) TOPOLOGY: linear
48        (ii) MOLECULE TYPE: cDNA
49
50        (ix) FEATURE:
51             (A) NAME/KEY: CDS
52             (B) LOCATION: 278..1047
53
54        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
55
56   TCCACATGGC TACAGGTAAG CGCCCCTAAA ATCCCTTTGG GCACAATGTG TCCTGAGGGG      60
57
58   AGAGGCAGCG ACCTGTAGAT GGGACGGGGG CACTAACCCT CAGGTTTGGG GCTTCTCAAT     120
59
60   CTCACTATCG CCATGTAAGC CCAGTATTTG GCCAATCTCA GAAAGCTCCT CCTCCCTGGA     180
61
62   GGGATGGAGA GAGAAAAACA AACAGCTCCT GGAGCAGGGA GAGTGCTGGC CTCTTGCTCT     240
63
64   CCGGCTCCCT CTGTTGCCCT CTGGTTTCTC CCCAGGC TCC CGG ACG TCC CTG CTC     295
65                                                Ser Arg Thr Ser Leu Leu
66                                                 1                   5
67
68   CTG GCT TTT GGC CTG CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT GCC     343
69   Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala
70                    10                  15                  20
71
72   GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCC     391
73   Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser
74            25                  30                  35
75
76   ATT TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT     439
77   Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
78        40                  45                  50
79
80   CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC     487
81   Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser
82   55                  60                  65                  70
83
84   TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA     535
85   Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys
86                    75                  80                  85
87
88   TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC     583
89   Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
90                    90                  95                 100
91
92   CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT TGG     631
93   Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp
94                   105                 110                 115
95
96   AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC AAT GGG     679
97   Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly
98        120                 125                 130
99
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INPUT SET: S16859.raw

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100    ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG TGC ACC TGC    727
101    Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys
102    135                 140                 145                 150

104    CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC TCC TGT GCC GGT    775
105    His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ala Gly
106                    155                 160                 165

108    GCT GCC CCA GGT TGC CCA GAA TGC ACG CTA CAG GAA AAC CCA TTC TTC    823
109    Ala Ala Pro Gly Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe
110                    170                 175                 180

112    TCC CAG CCG GGT GCC CCA ATA CTT CAG TGC ATG GGC TGC TGC TTC TCT    871
113    Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser
114                    185                 190                 195

116    AGA GCA TAT CCC ACT CCA CTA AGG TCC AAG AAG ACG ATG TTG GTC CAA    919
117    Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln
118        200                 205                 210

120    AAG AAC GTC ACC TCA GAG TCC ACT TGC TGT GTA GCT AAA TCA TAT AAC    967
121    Lys Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn
122    215                 220                 225                 230

124    AGG GTC ACA GTC ATG GGG GGT TTC AAA GTG GAG AAC CAC ACG GGG TGC    1015
125    Arg Val Thr Val Met Gly Gly Phe Lys Val Glu Asn His Thr Gly Cys
126                    235                 240                 245

128    CAC TGC AGT ACT TGT TAT TAT CAC AAA TCT  TA AG                      1049
129    His Cys Ser Thr Cys Tyr Tyr His Lys Ser
130                    250                 255
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(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 256 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp
  1               5                  10                  15

Leu Gln Glu Gly Ser Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile
              20              25                  30

His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr
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INPUT SET: S16859.raw

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153                35                    40                    45
154
155    Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg
156         50                  55                  60
157
158    Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His
159     65                  70                  75                  80
160
161    Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile
162                  85                  90                  95
163
164    Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn
165              100                 105                 110
166
167    Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys
168         115                 120                 125
169
170    Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln
171         130                 135                 140
172
173    Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu
174    145                 150                 155                 160
175
176    Cys Val Ser Cys Ala Gly Ala Ala Pro Gly Cys Pro Glu Cys Thr Leu
177              165                 170                 175
178
179    Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys
180              180                 185                 190
181
182    Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys
183         195                 200                 205
184
185    Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu Ser Thr Cys Cys
186         210                 215                 220
187
188    Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly Phe Lys Val
189    225                 230                 235                 240
190
191    Glu Asn His Thr Gly Cys His Cys Ser Thr Cys Tyr Tyr His Lys Ser
192              245                 250                 255
193
194
195    (2) INFORMATION FOR SEQ ID NO:3:
196
197         (i) SEQUENCE CHARACTERISTICS:
198              (A) LENGTH: 1202 base pairs
199              (B) TYPE: nucleic acid
200              (C) STRANDEDNESS: single
201              (D) TOPOLOGY: linear
202
203         (ii) MOLECULE TYPE: cDNA
204
205         (ix) FEATURE:
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RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/804,166*

INPUT SET: S16859.raw

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206              (A) NAME/KEY: CDS
207              (B) LOCATION: 279..1199
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209       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
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211   CTCGAGATGG CTACAGGTAA GCGCCCCTAA AATCCCTTTG GGCACAATGT GTCCTGAGGG        60
212
213   GAGAGGTAGC GACCTGTAGA TGGGACGGGG GCACTAACCC TGAGGTTTGG GGCTTCTGAA       120
214
215   TGTGAGTATC GCCATGTAAG CCCAGTATTT GGCCAATGTC AGAAAGCTCC TGGTCCCTGG       180
216
217   AGGGATGGAG AGAGAAAAAC AAACAGCTCC TGGAGCAGGG AGAGTGCTGG CCTCTTGCTC       240
218
219   TCCGGCTCCC TCTGTTGCCC TGTGGTTTCT CCCCAGGC TCC CGG ACG TCC CTG          293
220                                                Ser Arg Thr Ser Leu
221                                                              260
222
223   CTC CTG GCT TTT GGC CTG CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT       341
224   Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser
225               265                 270                 275
226
227   GCC GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT       389
228   Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn
229               280                 285                 290
230
231   TCG ATT TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC       437
232   Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp
233       295                 300                 305
234
235   TGT CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC       485
236   Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly
237   310                 315                 320                 325
238
239   TCT TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC       533
240   Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser
241               330                 335                 340
242
243   AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG       581
244   Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val
245               345                 350                 355
246
247   GAC CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT       629
248   Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr
249               360                 365                 370
250
251   TGG AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC AAT       677
252   Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn
253       375                 380                 385
254
255   GGG ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG TGC ACC       725
256   Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr
257   390                 395                 400                 405
258
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SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION *US/08/804,166*

INPUT SET: S16859.raw

APPLICATION NUMBER
FILING DATE
CLASSIFICATION
CURRENT APPLICATION DATA

Serial Number: 08/804,166

CRF Processing Date: 4/10/97
Edited by: _____ A
Verified by: _____ AL _____ (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically: _____

ENTERED

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____ .

☑ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included: _____

☐ Deleted extra, invalid, headings used by an applicant, specifically: _____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____ .

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically: _____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically: _____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other: _____

_____

_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.   3/1/95

TEAM 3

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/804,166*

DATE: 04/10/97
TIME: 17:05:27

INPUT SET: S16859.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

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 1                              SEQUENCE LISTING
 2
 3   (1)    General Information:
 4
 5       (i) APPLICANT: Campbell, Robert K.
 6                      Jameson, Bradford A.
 7                      Chappel, Scott C.
 8
 9      (ii) TITLE OF INVENTION: HYBRID PROTEINS
10
11     (iii) NUMBER OF SEQUENCES: 22
12
13      (iv) CORRESPONDENCE ADDRESS:
14           (A) ADDRESSEE: BROWDY AND NEIMARK
15           (B) STREET: 419 Seventh Street N.W., Ste. 300
16           (C) CITY: Washington
17           (D) STATE: D.C.
18           (E) COUNTRY: USA
19           (F) ZIP: 22207
20
21       (v) COMPUTER READABLE FORM:
22           (A) MEDIUM TYPE: Floppy disk
23           (B) COMPUTER: IBM PC compatible
24           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25           (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26
27      (vi) CURRENT APPLICATION DATA:
28           (A) APPLICATION NUMBER:
29           (B) FILING DATE:
30           (C) CLASSIFICATION:
31
32     (vii) PRIOR APPLICATION DATA:
33           (A) APPLICATION NUMBER:  60/011,936
34           (B) FILING DATE:  20 February 1996
35           (C) CLASSIFICATION:
36
37    (viii) ATTORNEY/AGENT INFORMATION:
38           (A) NAME: Browdy, Roger L.
39           (B) REGISTRATION NUMBER: 25,618
40           (C) REFERENCE/DOCKET NUMBER: CAMPBELL=2A
41
42      (ix) TELECOMMUNICATION INFORMATION:
43           (A) TELEPHONE: (202) 628-5197
44           (B) TELEFAX: (202) 737-3528
45
46   (2) INFORMATION FOR SEQ ID NO:1:
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INPUT SET: S16859.raw

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47
48        (i) SEQUENCE CHARACTERISTICS:
49             (A) LENGTH: 1049 base pairs
50             (B) TYPE: nucleic acid
51             (C) STRANDEDNESS: single
52             (D) TOPOLOGY: linear
53        (ii) MOLECULE TYPE: cDNA
54
55        (ix) FEATURE:
56             (A) NAME/KEY: CDS
57             (B) LOCATION: 278..1047
58
59        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
60
61 TCCACATGGC TACAGGTAAG CGCCCCTAAA ATCCCTTTGG GCACAATGTG TCCTGAGGGG          60
62
63 AGAGGCAGCG ACCTGTAGAT GGGACGGGGG CACTAACCCT CAGGTTTGGG GCTTCTCAAT         120
64
65 CTCACTATCG CCATGTAAGC CCAGTATTTG GCCAATCTCA GAAAGCTCCT CCTCCCTGGA         180
66
67 GGGATGGAGA GAGAAAAACA AACAGCTCCT GGAGCAGGGA GAGTGCTGGC CTCTTGCTCT         240
68
69 CCGGCTCCCT CTGTTGCCCT CTGGTTTCTC CCCAGGC TCC CGG ACG TCC CTG CTC         295
70                                         Ser Arg Thr Ser Leu Leu
71                                           1               5
72
73 CTG GCT TTT GGC CTG CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT GCC         343
74 Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala
75             10                  15                  20
76
77 GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCC         391
78 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser
79          25                  30                  35
80
81 ATT TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT         439
82 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
83       40                  45                  50
84
85 CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC         487
86 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser
87  55                  60                  65                  70
88
89 TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA         535
90 Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys
91                  75                  80                  85
92
93 TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC         583
94 Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
95          90                  95                 100
96
97 CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT TGG         631
98 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp
99         105                 110                 115
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101    AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC AAT GGG        679
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103        120                     125                 130
104
105    ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG TGC ACC TGC        727
106    Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys
107    135                     140                 145                 150
108
109    CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC TCC TGT GCC GGT        775
110    His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ala Gly
111                    155                 160                 165
112
113    GCT GCC CCA GGT TGC CCA GAA TGC ACG CTA CAG GAA AAC CCA TTC TTC        823
114    Ala Ala Pro Gly Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe
115                    170                 175                 180
116
117    TCC CAG CCG GGT GCC CCA ATA CTT CAG TGC ATG GGC TGC TGC TTC TCT        871
118    Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser
119                    185                 190                 195
120
121    AGA GCA TAT CCC ACT CCA CTA AGG TCC AAG AAG ACG ATG TTG GTC CAA        919
122    Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln
123        200                     205                 210
124
125    AAG AAC GTC ACC TCA GAG TCC ACT TGC TGT GTA GCT AAA TCA TAT AAC        967
126    Lys Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn
127    215                     220                 225                 230
128
129    AGG GTC ACA GTC ATG GGG GGT TTC AAA GTG GAG AAC CAC ACG GGG TGC       1015
130    Arg Val Thr Val Met Gly Gly Phe Lys Val Glu Asn His Thr Gly Cys
131                    235                 240                 245
132
133    CAC TGC AGT ACT TGT TAT TAT CAC AAA TCT   TA AG                       1049
134    His Cys Ser Thr Cys Tyr Tyr His Lys Ser
135                    250                 255
136
137
138
139
140    (2) INFORMATION FOR SEQ ID NO:2:
141
142           (i) SEQUENCE CHARACTERISTICS:
143                  (A) LENGTH: 256 amino acids
144                  (B) TYPE: amino acid
145                  (D) TOPOLOGY: linear
146
147           (ii) MOLECULE TYPE: protein
148
149           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
150
151    Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp
152      1                 5                  10                  15
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153
154   Leu Gln Glu Gly Ser Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile
155               20                  25                  30
156
157   His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr
158               35                  40                  45
159
160   Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg
161        50                  55                  60
162
163   Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His
164    65                  70                  75                  80
165
166   Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile
167               85                  90                  95
168
169   Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn
170               100                 105                 110
171
172   Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys
173        115                 120                 125
174
175   Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln
176        130                 135                 140
177
178   Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu
179    145                 150                 155                 160
180
181   Cys Val Ser Cys Ala Gly Ala Ala Pro Gly Cys Pro Glu Cys Thr Leu
182               165                 170                 175
183
184   Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys
185               180                 185                 190
186
187   Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys
188        195                 200                 205
189
190   Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu Ser Thr Cys Cys
191        210                 215                 220
192
193   Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly Phe Lys Val
194    225                 230                 235                 240
195
196   Glu Asn His Thr Gly Cys His Cys Ser Thr Cys Tyr Tyr His Lys Ser
197               245                 250                 255
198
199                                                       •
200   (2) INFORMATION FOR SEQ ID NO:3:
201                                                  ◢
202        (i) SEQUENCE CHARACTERISTICS:
203             (A) LENGTH: 1202 base pairs         •
204             (B) TYPE: nucleic acid
205             (C) STRANDEDNESS: single
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206              (D) TOPOLOGY: linear
207
208        (ii) MOLECULE TYPE: cDNA
209
210        (ix) FEATURE:
211             (A) NAME/KEY: CDS
212             (B) LOCATION: 279..1199
213
214        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
215
216    CTCGAGATGG CTACAGGTAA GCGCCCCTAA AATCCCTTTG GGCACAATGT GTCCTGAGGG      60
217
218    GAGAGGTAGC GACCTGTAGA TGGGACGGGG GCACTAACCC TGAGGTTTGG GGCTTCTGAA     120
219
220    TGTGAGTATC GCCATGTAAG CCCAGTATTT GGCCAATGTC AGAAAGCTCC TGGTCCCTGG     180
221
222    AGGGATGGAG AGAGAAAAAC AAACAGCTCC TGGAGCAGGG AGAGTGCTGG CCTCTTGCTC     240
223
224    TCCGGCTCCC TCTGTTGCCC TGTGGTTTCT CCCCAGGC TCC CGG ACG TCC CTG        293
225                                              Ser Arg Thr Ser Leu
226                                                              260
227
228    CTC CTG GCT TTT GGC CTG CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT     341
229    Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser
230                265                 270                 275
231
232    GCC GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT     389
233    Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn
234                280                 285                 290
235
236    TCG ATT TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC     437
237    Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp
238                295                 300                 305
239
240    TGT CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC     485
241    Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly
242    310                 315                 320                 325
243
244    TCT TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC     533
245    Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser
246                330                 335                 340
247
248    AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG     581
249    Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val
250                345                 350                 355
251
252    GAC CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT     629
253    Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr
254                360                 365                 370
255
256    TGG AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC AAT     677
257    Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn
258    375                 380                 385
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SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION   *US/08/804,166*

INPUT SET: S16859.raw

< < THERE ARE NO ITEMS MISSING > >